

SEQUENCE LISTING

<110> Kornbluth, Richard S
 <120> Multimeric forms of CD40L and other TNF family members
 <130> TNFSF-collectin fusion proteins
 <140> 60/111,471
 <141> 1998-12-08
 <160> 6
 <170> PatentIn Ver. 2.1
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 <222> (7)..(31)
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 <222> (88)..(799)
 <223> Mature murine surfactant protein D including hub
 region, collagenous portion, and neck, but
 excluding carbohydrate recognition domain (CRD)
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 <222> (801)..(1546)
 <223> Human CD40 ligand extracellular region, including
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 <221> sig_peptide
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 <223> Signal peptide from murine surfactant protein D
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 <223> Description of Artificial Sequence: Murine

surfactant protein D (without the CRD) fused to
the extracellular portion of human CD40L

<300>

<301> Spriggs, Melanie K.
Armitage, Richard J.
Strockbine, L
Clifford, K N.
Macduff, B M.
Sato, T A.
Maliszewski, C R.
Fanslow, William C.

<302> Recombinant human CD40 ligand stimulates B cell
proliferation and immunoglobulin E secretion.

<303> J. Exp. Med.

<304> 176

<305> 6

<306> 1543-1550

<307> 1992

<313> 801 TO 1600

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<301> Motwani, M
White, R A.

<302> Mouse surfactant protein-D. cDNA cloning,
characterization, and gene localization to chromosome
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<303> J. Immunol.

<304> 155

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<306> 5671-5677

<307> 1995

<313> 32 TO 800

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Leu Val Leu Leu Val Gln Pro Leu Gly Asn Leu Gly Ala Glu Met Lys
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Ser Leu Ser Gln Arg Ser Val Pro Asn Thr Cys Thr Leu Val Met Cys
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 the extracellular portion of human CD40L

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Thr Cys Thr Leu Val Met Cys Ser Pro Thr Glu Asn Gly Leu Pro Gly
 35 40 45

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Pro Gly Leu Pro Gly Pro Met Gly Leu Ser Gly Leu Gln Gly Pro Thr
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Pro Lys Gly Glu Arg Gly Leu Ser Gly Pro Pro Gly Leu Pro Gly Ile
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Thr Gly Pro Lys Gly Glu Arg Gly Ala Pro Gly Val Gln Gly Ala Pro
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Ala Leu Arg Gln Gln Met Glu Ala Leu Lys Gly Lys Leu Gln Arg Leu
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Glu Val Ala Phe Ser His Tyr Gln Lys Ala Ala Leu Phe Pro Asp Gly
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His Arg Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp
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Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe
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Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser
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Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val
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Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu
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Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln
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 carbohydrate recognition domain (CRD)

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 including stalk
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 White, R A.
 Guo, N
 Dowler, L L.
 Tauber, A I.
 Motwani, M
 <302> Mouse surfactant protein-D. cDNA cloning,
 characterization, and gene localization to chromosome
 14.
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 <304> 155
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 <306> 5671-5677
 <307> 1995
 <313> 32 TO 800

<300>
 <301> Anderson, D M.
 Maraskovsky, E
 Billingsley, W L.
 Dougall, W C.
 <302> A homologue of the TNF receptor and its ligand enhance
 T-cell growth and dendritic-cell function.
 <303> Nature
 <304> 390
 <305> 6656
 <306> 175-179
 <307> 1997
 <313> 801 TO 1534

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Pro Gly Asp Arg Gly Ile Lys Gly Glu Ser Gly Leu Pro Asp Ser Ala
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Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr Leu
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 385 390 395 400

Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val Pro
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Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn Trp
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 surfactant protein D (except CRD) fused to the
 extracellular domain of murine CD40 ligand

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 <223> 5' UTR from rat surfactant protein D

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 <223> Mature murine surfactant protein D including hub
 region, collagenous portion, and neck, but
 excluding carbohydrate recognition domain (CRD)

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 <223> Murine CD40 ligand extracellular region, including
 stalk

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 characterization, and gene localization to chromosome
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 <307> 1995
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 Fanslow, W
 Sato, T A.
 Clifford, K N.
 <302> Molecular and biological characterization of a murine
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 <303> Nature
 <304> 357

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 <306> 80-82
 <307> 1992
 <313> 801 TO 1441

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gctagcgaat tccaccagga agcaatctga c atg ctg ccc ttt ctc tcc atg	52
Met Leu Pro Phe Leu Ser Met	
1 5	
ctt gtc ttg ctt gta cag ccc ctg gga aat ctg gga gca gaa atg aag	100
Leu Val Leu Leu Val Gln Pro Leu Gly Asn Leu Gly Ala Glu Met Lys	
10 15 20	
agc ctc tcg cag aga tca gta ccc aac acc tgc acc cta gtc atg tgt	148
Ser Leu Ser Ser Gln Arg Ser Val Pro Asn Thr Cys Thr Leu Val Met Cys	
25 30 35	
agc cca aca gag aat ggc ctg cct ggt cgt gat gga cgg gat ggg aga	196
Ser Pro Thr Glu Asn Gly Leu Pro Gly Arg Asp Gly Arg Asp Gly Arg	
40 45 50 55	
gaa ggt cca cgg ggt gag aag ggt gat cca ggt ttg cca gga cct atg	244
Glu Gly Pro Arg Gly Glu Lys Gly Asp Pro Gly Leu Pro Gly Pro Met	
60 65 70	
ggg ctc tca ggg ttg cag ggc cct aca ggt cca gtt gga ccc aaa gga	292
Gly Leu Ser Gly Leu Gln Gly Pro Thr Gly Pro Val Gly Pro Lys Gly	
75 80 85	
gag aat ggc tct gct ggc gaa cct gga cca aag gga gaa cgt gga cta	340
Glu Asn Gly Ser Ala Gly Glu Pro Gly Pro Lys Gly Glu Arg Gly Leu	
90 95 100	
agt gga cct cca gga ctt cca ggt att cct ggt cca gct ggg aaa gaa	388
Ser Gly Pro Pro Gly Leu Pro Gly Ile Pro Gly Pro Ala Gly Lys Glu	
105 110 115	
ggt ccc tct ggg aag cag ggg aac ata gga cct caa ggc aaa cca ggt	436
Gly Pro Ser Gly Lys Gln Gly Asn Ile Gly Pro Gln Gly Lys Pro Gly	
120 125 130 135	
cct aaa gga gag gct ggg ccc aaa gga gaa gta ggt gct cct ggc atg	484
Pro Lys Gly Glu Ala Gly Pro Lys Gly Glu Val Gly Ala Pro Gly Met	
140 145 150	
caa gga tct aca ggg gca aaa ggc tcc aca ggc ccc aag gga gaa aga	532
Gln Gly Ser Thr Gly Ala Lys Gly Ser Thr Gly Pro Lys Gly Glu Arg	

155	160	165	
ggt gcc cct ggt gtg caa gga gcc cca ggg aat gct gga gca gca gga			580
Gly Ala Pro Gly Val Gln Gly Ala Pro Gly Asn Ala Gly Ala Ala Gly			
170	175	180	
cct gcc gga cct gcc ggt cca cag gga gct cca ggt tcc agg ggg ccc			628
Pro Ala Gly Pro Ala Gly Pro Gln Gly Ala Pro Gly Ser Arg Gly Pro			
185	190	195	
cca gga ctc aag ggg gac aga ggt gtt cct gga gac aga gga atc aaa			676
Pro Gly Leu Lys Gly Asp Arg Gly Val Pro Gly Asp Arg Gly Ile Lys			
200	205	210	215
ggt gaa agc ggg ctt cca gac agt gct gct ctg agg cag cag atg gag			724
Gly Glu Ser Gly Leu Pro Asp Ser Ala Ala Leu Arg Gln Gln Met Glu			
220	225	230	
gcc tta aaa gga aaa cta cag cgt cta gag gtt gcc ttc tcc cac tat			772
Ala Leu Lys Gly Lys Leu Gln Arg Leu Glu Val Ala Phe Ser His Tyr			
235	240	245	
cag aaa gct gca ttg ttc cct gat ggc cat aga aga ttg gat aag gtc			820
Gln Lys Ala Ala Leu Phe Pro Asp Gly His Arg Arg Leu Asp Lys Val			
250	255	260	
gaa gag gaa gta aac ctt cat gaa gat ttt gta ttc ata aaa aag cta			868
Glu Glu Glu Val Asn Leu His Glu Asp Phe Val Phe Ile Lys Lys Leu			
265	270	275	
aag aga tgc aac aaa gga gaa gga tct tta tcc ttg ctg aac tgt gag			916
Lys Arg Cys Asn Lys Gly Glu Gly Ser Leu Ser Leu Leu Asn Cys Glu			
280	285	290	295
gag atg aga agg caa ttt gaa gac ctt gtc aag gat ata acg tta aac			964
Glu Met Arg Arg Gln Phe Glu Asp Leu Val Lys Asp Ile Thr Leu Asn			
300	305	310	
aaa gaa gag aaa aaa gaa aac agc ttt gaa atg caa aga ggt gat gag			1012
Lys Glu Glu Lys Lys Glu Asn Ser Phe Glu Met Gln Arg Gly Asp Glu			
315	320	325	
gat cct caa att gca gca cac gtt gta agc gaa gcc aac agt aat gca			1060
Asp Pro Gln Ile Ala Ala His Val Val Ser Glu Ala Asn Ser Asn Ala			
330	335	340	
gca tcc gtt cta cag tgg gcc aag aaa gga tat tat acc atg aaa agc			1108
Ala Ser Val Leu Gln Trp Ala Lys Lys Gly Tyr Tyr Thr Met Lys Ser			

345

350

355

aac ttg gta atg ctt gaa aat ggg aaa cag ctg acg gtt aaa aga gaa 1156
 Asn Leu Val Met Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Glu
 360 365 370 375

gga ctc tat tat gtc tac act caa gtc acc ttc tgc tct aat cgg gag 1204
 Gly Leu Tyr Tyr Val Tyr Thr Gln Val Thr Phe Cys Ser Asn Arg Glu
 380 385 390

cct tcg agt caa cgc cca ttc atc gtc ggc ctc tgg ctg aag ccc agc 1252
 Pro Ser Ser Gln Arg Pro Phe Ile Val Gly Leu Trp Leu Lys Pro Ser
 395 400 405

att gga tct gag aga atc tta ctc aag gcg gca aat acc cac agt tcc 1300
 Ile Gly Ser Glu Arg Ile Leu Leu Lys Ala Ala Asn Thr His Ser Ser
 410 415 420

tcc cag ctt tgc gag cag cag tct gtt cac ttg ggc gga gtg ttt gaa 1348
 Ser Gln Leu Cys Glu Gln Gln Ser Val His Leu Gly Gly Val Phe Glu
 425 430 435

tta caa gct ggt gct tct gtg ttt gtc aac gtg act gaa gca agc caa 1396
 Leu Gln Ala Gly Ala Ser Val Phe Val Asn Val Thr Glu Ala Ser Gln
 440 445 450 455

gtg atc cac aga gtt ggc ttc tca tct ttt ggc tta ctc aaa ctc 1441
 Val Ile His Arg Val Gly Phe Ser Ser Phe Gly Leu Leu Lys Leu
 460 465 470

tgaacagtgc gctgtcctag gctgcagcag ggtacc 1477

<210> 6

<211> 470

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Murine
 surfactant protein D (except CRD) fused to the
 extracellular domain of murine CD40 ligand

<400> 6

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 1 5 10 15

Asn Leu Gly Ala Glu Met Lys Ser Leu Ser Gln Arg Ser Val Pro Asn
 20 25 30

Thr Cys Thr Leu Val Met Cys Ser Pro Thr Glu Asn Gly Leu Pro Gly
 35 40 45

Arg Asp Gly Arg Asp Gly Arg Glu Gly Pro Arg Gly Glu Lys Gly Asp
 50 55 60

Pro Gly Leu Pro Gly Pro Met Gly Leu Ser Gly Leu Gln Gly Pro Thr
 65 70 75 80

Gly Pro Val Gly Pro Lys Gly Glu Asn Gly Ser Ala Gly Glu Pro Gly
 85 90 95

Pro Lys Gly Glu Arg Gly Leu Ser Gly Pro Pro Gly Leu Pro Gly Ile
 100 105 110

Pro Gly Pro Ala Gly Lys Glu Gly Pro Ser Gly Lys Gln Gly Asn Ile
 115 120 125

Gly Pro Gln Gly Lys Pro Gly Pro Lys Gly Glu Ala Gly Pro Lys Gly
 130 135 140

Glu Val Gly Ala Pro Gly Met Gln Gly Ser Thr Gly Ala Lys Gly Ser
 145 150 155 160

Thr Gly Pro Lys Gly Glu Arg Gly Ala Pro Gly Val Gln Gly Ala Pro
 165 170 175

Gly Asn Ala Gly Ala Ala Gly Pro Ala Gly Pro Ala Gly Pro Gln Gly
 180 185 190

Ala Pro Gly Ser Arg Gly Pro Pro Gly Leu Lys Gly Asp Arg Gly Val
 195 200 205

Pro Gly Asp Arg Gly Ile Lys Gly Glu Ser Gly Leu Pro Asp Ser Ala
 210 215 220

Ala Leu Arg Gln Gln Met Glu Ala Leu Lys Gly Lys Leu Gln Arg Leu
 225 230 235 240

Glu Val Ala Phe Ser His Tyr Gln Lys Ala Ala Leu Phe Pro Asp Gly
 245 250 255

His Arg Arg Leu Asp Lys Val Glu Glu Glu Val Asn Leu His Glu Asp
 260 265 270

Phe Val Phe Ile Lys Lys Leu Lys Arg Cys Asn Lys Gly Glu Gly Ser
 275 280 285

Leu Ser Leu Leu Asn Cys Glu Glu Met Arg Arg Gln Phe Glu Asp Leu
 290 295 300

Val Lys Asp Ile Thr Leu Asn Lys Glu Glu Lys Lys Glu Asn Ser Phe
 305 310 315 320

Glu Met Gln Arg Gly Asp Glu Asp Pro Gln Ile Ala Ala His Val Val
 325 330 335

Ser Glu Ala Asn Ser Asn Ala Ala Ser Val Leu Gln Trp Ala Lys Lys
 340 345 350

Gly Tyr Tyr Thr Met Lys Ser Asn Leu Val Met Leu Glu Asn Gly Lys
 355 360 365

Gln Leu Thr Val Lys Arg Glu Gly Leu Tyr Tyr Val Tyr Thr Gln Val
 370 375 380

Thr Phe Cys Ser Asn Arg Glu Pro Ser Ser Gln Arg Pro Phe Ile Val
 385 390 395 400

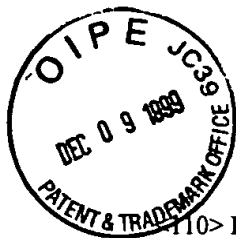
Gly Leu Trp Leu Lys Pro Ser Ile Gly Ser Glu Arg Ile Leu Leu Lys
 405 410 415

Ala Ala Asn Thr His Ser Ser Ser Gln Leu Cys Glu Gln Gln Ser Val
 420 425 430

His Leu Gly Gly Val Phe Glu Leu Gln Ala Gly Ala Ser Val Phe Val
 435 440 445

Asn Val Thr Glu Ala Ser Gln Val Ile His Arg Val Gly Phe Ser Ser
 450 455 460

Phe Gly Leu Leu Lys Leu
 465 470



12.13.99

SEQUENCE LISTING

<110> Kornbluth, Richard S

<120> Multimeric forms of CD40L and other TNF family members

<130> TNFSF-collectin fusion proteins

<140> 60/111,471

<141> 1998-12-08

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 1552

<212> DNA

<213> Artificial Sequence

<220>

<221> 5'UTR

<222> (7)..(31)

<220>

<221> misc_feature

<222> (88)..(799)

<223> Mature murine surfactant protein D including hub region, collagenous portion, and neck, but excluding carbohydrate recognition domain (CRD)

<220>

<221> misc_feature

<222> (801)..(1546)

<223> Human CD40 ligand extracellular region, including stalk.

<220>

<221> sig_peptide

<222> (32)..(88)

<223> Signal peptide from murine surfactant protein D

<220>

<221> CDS

<222> (32)..(1444)

<220>

<223> Description of Artificial Sequence: Murine surfactant protein D (without the CRD) fused to the extracellular portion of human CD40L

<300>

<301> Spriggs, Melanie K.
Armitage, Richard J.

Strockbine, L
Clifford, K N.
Macduff, B M.
Sato, T A.
Maliszewski, C R.
Fanslow, William C.

<302> Recombinant human CD40 ligand stimulates B cell
proliferation and immunoglobulin E secretion.

<303> J. Exp. Med.

<304> 176

<305> 6

<306> 1543-1550

<307> 1992

<313> 801 TO 1600

<300>

<301> Motwani, M

White, R A.

<302> Mouse surfactant protein-D. cDNA cloning,
characterization, and gene localization to chromosome
14.

<303> J. Immunol.

<304> 155

<305> 12

<306> 5671-5677

<307> 1995

<313> 32 TO 800

<400> 1

gctagcgaat tccaccagga agcaatctga c atg ctg ccc ttt ctc tcc atg 52

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1 5

ctt gtc ttg ctt gta cag ccc ctg gga aat ctg gga gca gaa atg aag 100

Leu Val Leu Leu Val Gln Pro Leu Gly Asn Leu Gly Ala Glu Met Lys

10 15 20

agc ctc tcg cag aga tca gta ccc aac acc tgc acc cta gtc atg tgt 148

Ser Leu Ser Gln Arg Ser Val Pro Asn Thr Cys Thr Leu Val Met Cys

25 30 35

agc cca aca gag aat ggc ctg cct ggt cgt gat gga cgg gat ggg aga 196

Ser Pro Thr Glu Asn Gly Leu Pro Gly Arg Asp Gly Arg Asp Gly Arg

40 45 50 55

gaa ggt cca cgg ggt gag aag ggt gat cca ggt ttg cca gga cct atg 244

Glu Gly Pro Arg Gly Glu Lys Gly Asp Pro Gly Leu Pro Gly Pro Met

60 65 70

ggg ctc tca ggg ttg cag ggc cct aca ggt cca gtt gga ccc aaa gga 292

Gly Leu Ser Gly Leu Gln Gly Pro Thr Gly Pro Val Gly Pro Lys Gly

75 80 85

gag aat ggc tct gct ggc gaa cct gga cca aag gga gaa cgt gga cta 340

Glu Asn Gly Ser Ala Gly Glu Pro Gly Pro Lys Gly Glu Arg Gly Leu
90 95 100

agt gga cct cca gga ctt cca ggt att cct ggt cca gct ggg aaa gaa 388
Ser Gly Pro Pro Gly Leu Pro Gly Ile Pro Gly Pro Ala Gly Lys Glu
105 110 115

ggt ccc tct ggg aag cag ggg aac ata gga cct caa ggc aaa cca ggt 436
Gly Pro Ser Gly Lys Gln Gly Asn Ile Gly Pro Gln Gly Lys Pro Gly
120 125 130 135

cct aaa gga gag gct ggg ccc aaa gga gaa gta ggt gct cct ggc atg 484
Pro Lys Gly Glu Ala Gly Pro Lys Gly Glu Val Gly Ala Pro Gly Met
140 145 150

caa gga tct aca ggg gca aaa ggc tcc aca ggc ccc aag gga gaa aga 532
Gln Gly Ser Thr Gly Ala Lys Gly Ser Thr Gly Pro Lys Gly Glu Arg
155 160 165

ggt gcc cct ggt gtg caa gga gcc cca ggg aat gct gga gca gca gga 580
Gly Ala Pro Gly Val Gln Gly Ala Pro Gly Asn Ala Gly Ala Ala Gly
170 175 180

cct gcc gga cct gcc ggt cca cag gga gct cca ggt tcc agg ggg ccc 628
Pro Ala Gly Pro Ala Gly Pro Gln Gly Ala Pro Gly Ser Arg Gly Pro
185 190 195

cca gga ctc aag ggg gac aga ggt gtt cct gga gac aga gga atc aaa 676
Pro Gly Leu Lys Gly Asp Arg Gly Val Pro Gly Asp Arg Gly Ile Lys
200 205 210 215

ggt gaa agc ggg ctt cca gac agt gct gct ctg agg cag cag atg gag 724
Gly Glu Ser Gly Leu Pro Asp Ser Ala Ala Leu Arg Gln Gln Met Glu
220 225 230

gcc tta aaa gga aaa cta cag cgt cta gag gtt gcc ttc tcc cac tat 772
Ala Leu Lys Gly Lys Leu Gln Arg Leu Glu Val Ala Phe Ser His Tyr
235 240 245

cag aaa gct gca ttg ttc cct gat ggc cat aga agg ttg gac aag ata 820
Gln Lys Ala Ala Leu Phe Pro Asp Gly His Arg Arg Leu Asp Lys Ile
250 255 260

gaa gat gaa agg aat ctt cat gaa gat ttt gta ttc atg aaa acg ata 868
Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val Phe Met Lys Thr Ile
265 270 275

cag aga tgc aac aca gga gaa aga tcc tta tcc tta ctg aac tgt gag 916
Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser Leu Leu Asn Cys Glu
280 285 290 295

gag att aaa agc cag ttt gaa ggc ttt gtg aag gat ata atg tta aac 964
Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys Asp Ile Met Leu Asn
300 305 310

aaa gag gag acg aag aaa gaa aac agc ttt gaa atg caa aaa ggt gat 1012
Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu Met Gln Lys Gly Asp
315 320 325

cag aat cct caa att gcg gca cat gtc ata agt gag gcc agc agt aaa 1060
Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser Lys
330 335 340

aca aca tct gtg tta cag tgg gct gaa aaa gga tac tac acc atg agc 1108
Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser
345 350 355

aac aac ttg gta acc ctg gaa aat ggg aaa cag ctg acc gtt aaa aga 1156
Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg
360 365 370 375

caa gga ctc tat tat atc tat gcc caa gtc acc ttc tgt tcc aat cgg 1204
Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg
380 385 390

gaa gct tcg agt caa gct cca ttt ata gcc agc ctc tgc cta aag tcc 1252
Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser
395 400 405

ccc ggt aga ttc gag aga atc tta ctc aga gct gca aat acc cac agt 1300
Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His Ser
410 415 420

tcc gcc aaa cct tgc ggg caa caa tcc att cac ttg gga gga gta ttt 1348
Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe
425 430 435

gaa ttg caa cca ggt gct tcg gtg ttt gtc aat gtg act gat cca agc 1396
Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser
440 445 450 455

caa gtg agc cat ggc act ggc ttc acg tcc ttt ggc tta ctc aaa ctc 1444
Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu
460 465 470

tgaacagtgt caccttcgag gctgtggtgg agctgacgct gggagtcttc ataatacagc 1504

acaggcttaa gcccaattat acactccaag gcatgtagaa ctggtacc 1552

<210> 2

<211> 471

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Murine
surfactant protein D (without the CRD) fused to
the extracellular portion of human CD40L

<400> 2

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1 5 10 15

Asn Leu Gly Ala Glu Met Lys Ser Leu Ser Gln Arg Ser Val Pro Asn
20 25 30

Thr Cys Thr Leu Val Met Cys Ser Pro Thr Glu Asn Gly Leu Pro Gly
35 40 45

Arg Asp Gly Arg Asp Gly Arg Glu Gly Pro Arg Gly Glu Lys Gly Asp
50 55 60

Pro Gly Leu Pro Gly Pro Met Gly Leu Ser Gly Leu Gln Gly Pro Thr
65 70 75 80

Gly Pro Val Gly Pro Lys Gly Glu Asn Gly Ser Ala Gly Glu Pro Gly
85 90 95

Pro Lys Gly Glu Arg Gly Leu Ser Gly Pro Pro Gly Leu Pro Gly Ile
100 105 110

Pro Gly Pro Ala Gly Lys Glu Gly Pro Ser Gly Lys Gln Gly Asn Ile
115 120 125

Gly Pro Gln Gly Lys Pro Gly Pro Lys Gly Glu Ala Gly Pro Lys Gly
130 135 140

Glu Val Gly Ala Pro Gly Met Gln Gly Ser Thr Gly Ala Lys Gly Ser
145 150 155 160

Thr Gly Pro Lys Gly Glu Arg Gly Ala Pro Gly Val Gln Gly Ala Pro
165 170 175

Gly Asn Ala Gly Ala Ala Gly Pro Ala Gly Pro Ala Gly Pro Gln Gly
180 185 190

Ala Pro Gly Ser Arg Gly Pro Pro Gly Leu Lys Gly Asp Arg Gly Val
195 200 205

Pro Gly Asp Arg Gly Ile Lys Gly Glu Ser Gly Leu Pro Asp Ser Ala
210 215 220

Ala Leu Arg Gln Gln Met Glu Ala Leu Lys Gly Lys Leu Gln Arg Leu
225 230 235 240

Glu Val Ala Phe Ser His Tyr Gln Lys Ala Ala Leu Phe Pro Asp Gly
245 250 255

His Arg Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp
260 265 270

Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser
275 280 285

Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe
290 295 300

Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser
305 310 315 320

Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val
325 330 335

Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu
340 345 350

Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly
355 360 365

Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln
370 375 380

Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile
385 390 395 400

Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu
405 410 415

Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser
420 425 430

Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe
435 440 445

Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr
450 455 460

Ser Phe Gly Leu Leu Lys Leu
465 470

<210> 3

<211> 1574

<212> DNA

<213> Artificial Sequence

<220>

<221> 5'UTR

<222> (7)..(31)

<223> 5' UTR taken from rat sequence for surfactant
protein D

<220>

<221> sig_peptide

<222> (32)..(88)

<223> Signal peptide from murine surfactant protein D

<220>
<221> CDS
<222> (32)..(1534)

<220>
<221> misc_feature
<222> (32)..(800)
<223> Murine surfactant protein D including hub region,
collagenous portion, and neck, but excluding
carbohydrate recognition domain (CRD)

<220>
<221> misc_feature
<222> (801)..(1534)
<223> Murine RANKL/TRANSE extracellular region,
including stalk

<300>
<301> Motwani, M
White, R A.
Guo, N
Dowler, L L.
Tauber, A I.
Motwani, M
<302> Mouse surfactant protein-D. cDNA cloning,
characterization, and gene localization to chromosome
14.
<303> J. Immunol.
<304> 155
<305> 12
<306> 5671-5677
<307> 1995
<313> 32 TO 800

<300>
<301> Anderson, D M.
Maraskovsky, E
Billingsley, W L.
Dougall, W C.
<302> A homologue of the TNF receptor and its ligand enhance
T-cell growth and dendritic-cell function.
<303> Nature
<304> 390
<305> 6656
<306> 175-179
<307> 1997
<313> 801 TO 1534

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gctagcgaat tccaccagga agcaatctga c atg ctg ccc ttt ctc tcc atg 52
Met Leu Pro Phe Leu Ser Met

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gcc tta aaa gga aaa cta cag cgt cta gag gtt gcc ttc tcc cac tat 772
 Ala Leu Lys Gly Lys Leu Gln Arg Leu Glu Val Ala Phe Ser His Tyr
 235 240 245

cag aaa gct gca ttg ttc cct gat ggt cga gcg cag atg gat cct aac 820
 Gln Lys Ala Ala Leu Phe Pro Asp Gly Arg Ala Gln Met Asp Pro Asn
 250 255 260

aga ata tca gaa gac agc act cac tgc ttt tat aga atc ctg aga ctc 868
 Arg Ile Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu
 265 270 275

cat gaa aac gca ggt ttg cag gac tcg act ctg gag agt gaa gac aca 916
 His Glu Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr
 280 285 290 295

cta cct gac tcc tgc agg agg atg aaa caa gcc ttt cag ggg gcc gtg 964
 Leu Pro Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val
 300 305 310

cag aag gaa ctg caa cac att gtg ggg cca cag cgc ttc tca gga gct 1012
 Gln Lys Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala
 315 320 325

cca gct atg atg gaa ggc tca tgg ttg gat gtg gcc cag cga ggc aag 1060
 Pro Ala Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys
 330 335 340

cct gag gcc cag cca ttt gca cac ctc acc atc aat gct gcc agc atc 1108
 Pro Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile
 345 350 355

cca tcg ggt tcc cat aaa gtc act ctg tcc tct tgg tac cac gat cga 1156
 Pro Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg
 360 365 370 375

ggc tgg gcc aag atc tct aac atg acg tta agc aac gga aaa cta agg 1204
 Gly Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg
 380 385 390

gtt aac caa gat ggc ttc tat tac ctg tac gcc aac att tgc ttt cgg 1252
 Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg
 395 400 405

cat cat gaa aca tcg gga agc gta cct aca gac tat ctt cag ctg atg 1300
 His His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met
 410 415 420

gtg tat gtc gtt aaa acc agc atc aaa atc cca agt tct cat aac ctg 1348
 Val Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu
 425 430 435

1000 900 800 700 600 500 400 300 200 100 0

atg aaa gga ggg agc acg aaa aac tgg tcg ggc aat tct gaa ttc cac 1396
Met Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His
440 445 450 455

ttt tat tcc ata aat gtt ggg gga ttt ttc aag ctc cga gct ggt gaa 1444
Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu
460 465 470

gaa att agc att cag gtg tcc aac cct tcc ctg ctg gat ccg gat caa 1492
Glu Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln
475 480 485

gat gcg acg tac ttt ggg gct ttc aaa gtt cag gac ata gac 1534
Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
490 495 500

tgagactcat ttcgtggaac attagcggcc gctaaactat 1574

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<211> 501
<212> PRT
<213> Artificial Sequence

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Thr Cys Thr Leu Val Met Cys Ser Pro Thr Glu Asn Gly Leu Pro Gly
35 40 45

Arg Asp Gly Arg Asp Gly Arg Glu Gly Pro Arg Gly Glu Lys Gly Asp
50 55 60

Pro Gly Leu Pro Gly Pro Met Gly Leu Ser Gly Leu Gln Gly Pro Thr
65 70 75 80

Gly Pro Val Gly Pro Lys Gly Glu Asn Gly Ser Ala Gly Glu Pro Gly
85 90 95

Pro Lys Gly Glu Arg Gly Leu Ser Gly Pro Pro Gly Leu Pro Gly Ile
100 105 110

Pro Gly Pro Ala Gly Lys Glu Gly Pro Ser Gly Lys Gln Gly Asn Ile
115 120 125

Gly Pro Gln Gly Lys Pro Gly Pro Lys Gly Glu Ala Gly Pro Lys Gly
130 135 140

Glu Val Gly Ala Pro Gly Met Gln Gly Ser Thr Gly Ala Lys Gly Ser
145 150 155 160

Thr Gly Pro Lys Gly Glu Arg Gly Ala Pro Gly Val Gln Gly Ala Pro
165 170 175

Gly Asn Ala Gly Ala Ala Gly Pro Ala Gly Pro Ala Gly Pro Gln Gly
180 185 190

Ala Pro Gly Ser Arg Gly Pro Pro Gly Leu Lys Gly Asp Arg Gly Val
195 200 205

Pro Gly Asp Arg Gly Ile Lys Gly Glu Ser Gly Leu Pro Asp Ser Ala
210 215 220

Ala Leu Arg Gln Gln Met Glu Ala Leu Lys Gly Lys Leu Gln Arg Leu
225 230 235 240

Glu Val Ala Phe Ser His Tyr Gln Lys Ala Ala Leu Phe Pro Asp Gly
245 250 255

Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His Cys
260 265 270

Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp Ser
275 280 285

Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met Lys
290 295 300

Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly
305 310 315 320

Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp Leu
325 330 335

Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His Leu
340 345 350

Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr Leu
355 360 365

Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr
370 375 380

Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr Leu
385 390 395 400

Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val Pro
405 410 415

Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile Lys
420 425 430

Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn Trp
435 440 445

Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe
450 455 460

Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn Pro
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Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys
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Val Gln Asp Ile Asp
500

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<211> 1477

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Murine
surfactant protein D (except CRD) fused to the
extracellular domain of murine CD40 ligand

<220>

<221> 5'UTR

<222> (7)..(31)

<223> 5' UTR from rat surfactant protein D

<220>

<221> sig_peptide

<222> (32)..(88)

<223> Signal peptide from murine surfactant protein D

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<221> CDS

<222> (32)..(1441)

<220>

<221> misc_recomb

<222> (88)..(799)

<223> Mature murine surfactant protein D including hub
region, collagenous portion, and neck, but
excluding carbohydrate recognition domain (CRD)

<220>

<221> misc_feature

<222> (800)..(1441)

<223> Murine CD40 ligand extracellular region, including
stalk

<300>

<301> Motwani, M

White, R A.
Guo, N
Dowler, L L.
Tauber, A I.
Motwani, M

<302> Mouse surfactant protein-D. cDNA cloning,
characterization, and gene localization to chromosome
14.

<303> J. Immunol.

<304> 155

<305> 12

<306> 5671-5677

<307> 1995

<313> 32 TO 800

<300>

<301> Armitage, R

Fanslow, W

Sato, T A.

Clifford, K N.

<302> Molecular and biological characterization of a murine
ligand for CD40

<303> Nature

<304> 357

<305> 6373

<306> 80-82

<307> 1992

<313> 801 TO 1441

<400> 5

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Met Leu Pro Phe Leu Ser Met

1 5

ctt gtc ttg ctt gta cag ccc ctg gga aat ctg gga gca gaa atg aag 100

Leu Val Leu Leu Val Gln Pro Leu Gly Asn Leu Gly Ala Glu Met Lys

10 15 20

agc ctc tcg cag aga tca gta ccc aac acc tgc acc cta gtc atg tgt 148

Ser Leu Ser Gln Arg Ser Val Pro Asn Thr Cys Thr Leu Val Met Cys

25 30 35

agc cca aca gag aat ggc ctg cct ggt cgt gat gga cgg gat ggg aga 196

Ser Pro Thr Glu Asn Gly Leu Pro Gly Arg Asp Gly Arg Asp Gly Arg

40 45 50 55

gaa ggt cca cgg ggt gag aag ggt gat cca ggt ttg cca gga cct atg 244

Glu Gly Pro Arg Gly Glu Lys Gly Asp Pro Gly Leu Pro Gly Pro Met

60 65 70

ggg ctc tca ggg ttg cag ggc cct aca ggt cca gtt gga ccc aaa gga 292

Gly Leu Ser Gly Leu Gln Gly Pro Thr Gly Pro Val Gly Pro Lys Gly

75 80 85

gag aat ggc tct gct ggc gaa cct gga cca aag gga gaa cgt gga cta 340
Glu Asn Gly Ser Ala Gly Glu Pro Gly Pro Lys Gly Glu Arg Gly Leu
90 95 100

agt gga cct cca gga ctt cca ggt att cct ggt cca gct ggg aaa gaa 388
Ser Gly Pro Pro Gly Leu Pro Gly Ile Pro Gly Pro Ala Gly Lys Glu
105 110 115

ggt ccc tct ggg aag cag ggg aac ata gga cct caa ggc aaa cca ggt 436
Gly Pro Ser Gly Lys Gln Gly Asn Ile Gly Pro Gln Gly Lys Pro Gly
120 125 130 135

cct aaa gga gag gct ggg ccc aaa gga gaa gta ggt gct cct ggc atg 484
Pro Lys Gly Glu Ala Gly Pro Lys Gly Glu Val Gly Ala Pro Gly Met
140 145 150

caa gga tct aca ggg gca aaa ggc tcc aca ggc ccc aag gga gaa aga 532
Gln Gly Ser Thr Gly Ala Lys Gly Ser Thr Gly Pro Lys Gly Glu Arg
155 160 165

ggt gcc cct ggt gtg caa gga gcc cca ggg aat gct gga gca gca gga 580
Gly Ala Pro Gly Val Gln Gly Ala Pro Gly Asn Ala Gly Ala Ala Gly
170 175 180

cct gcc gga cct gcc ggt cca cag gga gct cca ggt tcc agg ggg ccc 628
Pro Ala Gly Pro Ala Gly Pro Gln Gly Ala Pro Gly Ser Arg Gly Pro
185 190 195

cca gga ctc aag ggg gac aga ggt gtt cct gga gac aga gga atc aaa 676
Pro Gly Leu Lys Gly Asp Arg Gly Val Pro Gly Asp Arg Gly Ile Lys
200 205 210 215

ggt gaa agc ggg ctt cca gac agt gct gct ctg agg cag cag atg gag 724
Gly Glu Ser Gly Leu Pro Asp Ser Ala Ala Leu Arg Gln Gln Met Glu
220 225 230

gcc tta aaa gga aaa cta cag cgt cta gag gtt gcc ttc tcc cac tat 772
Ala Leu Lys Gly Lys Leu Gln Arg Leu Glu Val Ala Phe Ser His Tyr
235 240 245

cag aaa gct gca ttg ttc cct gat ggc cat aga aga ttg gat aag gtc 820
Gln Lys Ala Ala Leu Phe Pro Asp Gly His Arg Arg Leu Asp Lys Val
250 255 260

gaa gag gaa gta aac ctt cat gaa gat ttt gta ttc ata aaa aag cta 868
Glu Glu Glu Val Asn Leu His Glu Asp Phe Val Phe Ile Lys Lys Leu
265 270 275

aag aga tgc aac aaa gga gaa gga tct tta tcc ttg ctg aac tgt gag 916
Lys Arg Cys Asn Lys Gly Glu Gly Ser Leu Ser Leu Leu Asn Cys Glu
280 285 290 295

gag atg aga agg caa ttt gaa gac ctt gtc aag gat ata acg tta aac 964
Glu Met Arg Arg Gln Phe Glu Asp Leu Val Lys Asp Ile Thr Leu Asn

300

305

310

aaa gaa gag aaa aaa gaa aac agc ttt gaa atg caa aga ggt gat gag 1012
 Lys Glu Glu Lys Lys Glu Asn Ser Phe Glu Met Gln Arg Gly Asp Glu
 315 320 325

gat cct caa att gca gca cac gtt gta agc gaa gcc aac agt aat gca 1060
 Asp Pro Gln Ile Ala Ala His Val Val Ser Glu Ala Asn Ser Asn Ala
 330 335 340

gca tcc gtt cta cag tgg gcc aag aaa gga tat tat acc atg aaa agc 1108
 Ala Ser Val Leu Gln Trp Ala Lys Lys Gly Tyr Tyr Thr Met Lys Ser
 345 350 355

aac ttg gta atg ctt gaa aat ggg aaa cag ctg acg gtt aaa aga gaa 1156
 Asn Leu Val Met Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Glu
 360 365 370 375

gga ctc tat tat gtc tac act caa gtc acc ttc tgc tct aat cgg gag 1204
 Gly Leu Tyr Tyr Val Tyr Thr Gln Val Thr Phe Cys Ser Asn Arg Glu
 380 385 390

cct tcg agt caa cgc cca ttc atc gtc ggc ctc tgg ctg aag ccc agc 1252
 Pro Ser Ser Gln Arg Pro Phe Ile Val Gly Leu Trp Leu Lys Pro Ser
 395 400 405

att gga tct gag aga atc tta ctc aag gcg gca aat acc cac agt tcc 1300
 Ile Gly Ser Glu Arg Ile Leu Leu Lys Ala Ala Asn Thr His Ser Ser
 410 415 420

tcc cag ctt tgc gag cag cag tct gtt cac ttg ggc gga gtg ttt gaa 1348
 Ser Gln Leu Cys Glu Gln Gln Ser Val His Leu Gly Gly Val Phe Glu
 425 430 435

tta caa gct ggt gct tct gtg ttt gtc aac gtg act gaa gca agc caa 1396
 Leu Gln Ala Gly Ala Ser Val Phe Val Asn Val Thr Glu Ala Ser Gln
 440 445 450 455

gtg atc cac aga gtt ggc ttc tca tct ttt ggc tta ctc aaa ctc 1441
 Val Ile His Arg Val Gly Phe Ser Ser Phe Gly Leu Leu Lys Leu
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tgaacagtgc gctgtcctag gctgcagcag ggtacc 1477

<210> 6

<211> 470

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Murine
 surfactant protein D (except CRD) fused to the
 extracellular domain of murine CD40 ligand

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Met Leu Pro Phe Leu Ser Met Leu Val Leu Val Gln Pro Leu Gly
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Asn Leu Gly Ala Glu Met Lys Ser Leu Ser Gln Arg Ser Val Pro Asn
20 25 30

Thr Cys Thr Leu Val Met Cys Ser Pro Thr Glu Asn Gly Leu Pro Gly
35 40 45

Arg Asp Gly Arg Asp Gly Arg Glu Gly Pro Arg Gly Glu Lys Gly Asp
50 55 60

Pro Gly Leu Pro Gly Pro Met Gly Leu Ser Gly Leu Gln Gly Pro Thr
65 70 75 80

Gly Pro Val Gly Pro Lys Gly Glu Asn Gly Ser Ala Gly Glu Pro Gly
85 90 95

Pro Lys Gly Glu Arg Gly Leu Ser Gly Pro Pro Gly Leu Pro Gly Ile
100 105 110

Pro Gly Pro Ala Gly Lys Glu Gly Pro Ser Gly Lys Gln Gly Asn Ile
115 120 125

Gly Pro Gln Gly Lys Pro Gly Pro Lys Gly Glu Ala Gly Pro Lys Gly
130 135 140

Glu Val Gly Ala Pro Gly Met Gln Gly Ser Thr Gly Ala Lys Gly Ser
145 150 155 160

Thr Gly Pro Lys Gly Glu Arg Gly Ala Pro Gly Val Gln Gly Ala Pro
165 170 175

Gly Asn Ala Gly Ala Ala Gly Pro Ala Gly Pro Ala Gly Pro Gln Gly
180 185 190

Ala Pro Gly Ser Arg Gly Pro Pro Gly Leu Lys Gly Asp Arg Gly Val
195 200 205

Pro Gly Asp Arg Gly Ile Lys Gly Glu Ser Gly Leu Pro Asp Ser Ala
210 215 220

Ala Leu Arg Gln Gln Met Glu Ala Leu Lys Gly Lys Leu Gln Arg Leu
225 230 235 240

Glu Val Ala Phe Ser His Tyr Gln Lys Ala Ala Leu Phe Pro Asp Gly
245 250 255

His Arg Arg Leu Asp Lys Val Glu Glu Glu Val Asn Leu His Glu Asp
260 265 270

Phe Val Phe Ile Lys Lys Leu Lys Arg Cys Asn Lys Gly Glu Gly Ser
275 280 285

